RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/983,672_
Source: _IFWO_
Date Processed by STIC: _8/19/04_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY** or,
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2 PROGRAM** ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04): U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/983,672_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
prevent "wrapping."

2_____Invalid Line Length   The rules require that a line **not exceed 72 characters** in length. This includes white spaces.

3_____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
Numbering   use **space characters**, instead.

4_____Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5_____Variable Length   Sequence(s)_1,2_ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
"bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7_____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences   Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
(NEW RULES)   <210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11_____Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n/Xaa   "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

RAW SEQUENCE LISTING   DATE: 08/19/2004
PATENT APPLICATION: **US/10/783,672**   TIME: 15:14:43

Input Set : **D:\53279-20003.00 - Seqlist.txt**
Output Set: **N:\CRF4\08192004\J783672.raw**

```
 4 <110> APPLICANT: EMERSON, Beverly M.
 5        KADAM, Shilpa B.
 7 <120> TITLE OF INVENTION: METHODS OF MODULATING GENE EXPRESSION
10 <130> FILE REFERENCE: 532792000300
12 <140> CURRENT APPLICATION NUMBER: US 10/783,672
13 <141> CURRENT FILING DATE: 2004-02-20
15 <150> PRIOR APPLICATION NUMBER: US 60/450,771
16 <151> PRIOR FILING DATE: 2003-02-26
18 <160> NUMBER OF SEQ ID NOS: 3
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 20
24 <212> TYPE: PRT
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: ZN_FING
29 <222> LOCATION: 1,9
30 <223> OTHER INFORMATION: Xaa = tyrosine or phenylalanine
32 <221> NAME/KEY: ZN_FING
33 <222> LOCATION: 2, 6-8, 10-14, 16-17
34 <223> OTHER INFORMATION: Xaa = any amino acid
```

W--> `36 <221> ZN_FING`
```
37 <222> LOCATION: 4
38 <223> OTHER INFORMATION: Xaa = any amino acid may be present 2-4 times
```
W--> `40 <221> ZN_FING`
```
41 <222> LOCATION: 19
42 <223> OTHER INFORMATION: Xaa = any amino acid may be present 3-4 times
```
W--> `44 <400> 1`
W--> `45 Xaa Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa`
```
46 1           5                   10                  15
47 Xaa His Xaa His
48             20
51 <210> SEQ ID NO: 2
52 <211> LENGTH: 42
53 <212> TYPE: PRT
54 <213> ORGANISM: Homo sapiens
56 <220> FEATURE:
57 <221> NAME/KEY: ZN_FING
58 <222> LOCATION: 2-3, 5-17, 19-20, 24-28, 30-38, 40-41
59 <223> OTHER INFORMATION: Xaa = any amino acid
61 <221> NAME/KEY: ZN_FING
62 <222> LOCATION: 22
63 <223> OTHER INFORMATION: Xaa = any amino acid may be present 14-15 times
```

Handwritten annotations: Does Not Comply Corrected Diskette Needed

Xaa can only represent a single amino acid (see item 5 on Error summary sheet)

see item 5

RAW SEQUENCE LISTING   DATE: 08/19/2004
PATENT APPLICATION: US/10/783,672   TIME: 15:14:43

Input Set : D:\53279-20003.00 - Seqlist.txt
Output Set: N:\CRF4\08192004\J783672.raw

```
--> 65 <400> 2
--> 66 Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    67 1               5                   10                  15
    68 Xaa Cys Xaa Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
    69             20                  25                  30
    70 Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys
    71         35                  40
    74 <210> SEQ ID NO: 3
    75 <211> LENGTH: 33
    76 <212> TYPE: PRT
    77 <213> ORGANISM: Homo sapiens
    79 <220> FEATURE:
    80 <221> NAME/KEY: DNA_BIND
    81 <222> LOCATION: 3-6, 13-14, 21, 29, 31
    82 <223> OTHER INFORMATION: Xaa = any amino acid
    84 <400> SEQUENCE: 3
--> 85 Lys Arg Xaa Xaa Xaa Xaa Arg Lys Ser Ala Gln Asn Xaa Xaa Ser Ala
    86 1               5                   10                  15
    87 Gln Ser Ala Gln Xaa Arg Lys Thr Ala Glu Asn Gln Xaa Arg Xaa Arg
    88             20                  25                  30
    89 Lys
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/19/2004
PATENT APPLICATION: US/10/783,672   TIME: 15:14:44

Input Set : D:\53279-20003.00 - Seqlist.txt
Output Set: N:\CRF4\08192004\J783672.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 1,2,4,6,7,8,9,10,11,12,13,14,16,17,19
Seq#:2; Xaa Pos. 2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,19,20,22,24,25,26,27
Seq#:2; Xaa Pos. 28,30,31,32,33,34,35,36,37,38,40,41
Seq#:3; Xaa Pos. 3,4,5,6,13,14,21,29,31

VERIFICATION SUMMARY   DATE: 08/19/2004
PATENT APPLICATION: **US/10/783,672**   TIME: 15:14:44

Input Set : **D:\53279-20003.00 - Seqlist.txt**
Output Set: **N:\CRF4\08192004\J783672.raw**

```
L:36 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:40 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:44 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:45 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
M:341 Repeated in SeqNo=1
L:65 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:66 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
M:341 Repeated in SeqNo=2
L:85 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
M:341 Repeated in SeqNo=3
```